

SEQUENCE LISTING

<110> Gerritsen, Mary
Sliwkowski, Mark X.

<120> ErbB4 ANTAGONISTS

<130> GENENT.072A2

<150> 60/229,679

<151> 2000-09-01

<150> 60/265,516

<151> 2001-01-31

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 5484

<212> DNA

<213> Homo sapiens

<400> 1

```
aattgtcagc acgggatctg agacttccaa aaaatgaagc cggcgacagc actttgggtc 60
tggttgagcc ttctcgtggc ggoggggacc gtccagccca gcgattctca gtcagtgtgt 120
gcaggaacgg agaataaact gagctctctc tctgacctgg aacagcagta ccgagccttg 180
cgcaagtact atgaaaactg tgaggttgct atgggcaacc tggagataac cagcattgag 240
cacaaccggg acctctcctt cctgcggtct gttcgagaag tcacaggcta cgtgttagtg 300
gctcttaatc agtttctgta cctgcctctg gagaatttac gcattattcg tgggacaaaa 360
ctttatgagg atcgatatgc cttggcaata tttttaaact acagaaaaga tggaaacttt 420
ggacttcaag aacttggtt aaagaacttg acagaaatcc taaatggttg agtctatgta 480
gaccagaaca aattcctttg ttatgcagac accattcatt ggcaagatat tgttcggaac 540
ccatggcctt ccaacttgac tcttggtgta acaaatggta gttcaggatg tggacgttgc 600
cataagtctt gtactggccg ttgctgggga cccacagaaa atcattgcc a gactttgaca 660
aggacggtgt gtgcagaaca atgtgacggc agatgctacg gaccttacgt cagtgactgc 720
tgccatcgag aatgtgctgg aggtgctcga ggacctaagg acacagactg ctttgccctgc 780
atgaatttca atgacagtgg agcatgtgtt actcagtgtc cccaaacctt tgtctacaat 840
ccaaccacct ttcaactgga gcacaatttc aatgcaaagt acacatatgg agcattctgt 900
gtcaagaaat gtccacataa ctttgtggta gattccagtt cttgtgtgcg tgcctgccct 960
agttccaaga tggaagtaga agaaaatggg attaaaatgt gtaaaccttg cactgacatt 1020
tgcccaaaag cttgtgatgg cattggcaca ggatcattga tgtcagctca gactgtggat 1080
tcagtaaca ttgacaaatt cataaactgt accaagatca atgggaattt gatctttcta 1140
gtcactggta ttcatgggga cccttacaat gcaattgaag ccatagacct agagaaactg 1200
aacgtctttc ggacagtcag agagataaca ggtttcctga acatacagtc atggccacca 1260
aacatgactg acttcagtgt tttttctaac ctggtgacca ttggtggaag agtactctat 1320
agtggcctgt ccttgcttat cctcaagcaa cagggcatca cctctctaca gttccagtcc 1380
ctgaaggaaa tcagcgcagg aaacatctat attactgaca acagcaacct gtgttattat 1440
cataccatta actggacaac actcttcagc acaatcaacc agagaatagt aatccgggac 1500
aacagaaaag ctgaaaattg tactgctgaa ggaatggtgt gcaaccatct gtgttccagt 1560
gatggctgtt ggggacctgg gccagaccaa tgtctgtcgt gtcgccgctt cagtagagga 1620
aggatctgca tagagtcttg taacctctat gatggtgaat ttcgggagtt tgagaatggc 1680
tccatctgtg tggagtgtga cccccagtgt gagaagatgg aagatggcct cctcacatgc 1740
catggaccgg gtcttgacaa ctgtacaaag tgctctcatt ttaaagatgg cccaaactgt 1800
```

104330704650

gttgaaaaat	gtccagatgg	cttacagggg	gcaaacagtt	tcattttcaa	gtatgctgat	1860
ccagatcggg	agtgccaccc	atgccatcca	aactgcaccc	aagggtgtaa	cggtcccact	1920
agtcatgact	gcattttacta	cccatggacg	ggccattcca	ctttaccaca	acatgctaga	1980
actcccttga	ttgcagctgg	agtaattggt	gggctcttca	ttctggtcac	tgtgggtctg	2040
acatttgctg	tttatgtttag	aaggaagagc	atcaaaaaga	aaagagcctt	gagaagattc	2100
ttggaacag	agttggtgga	accattaact	cccagtgcca	cagcacccaa	tcaagctcaa	2160
cttcgtattt	tgaagaaaac	tgagctgaag	agggtaaaag	tccttggtct	aggtgctttt	2220
ggaacggttt	ataaaggtat	ttgggtacct	gaaggagaaa	ctgtgaagat	tcctgtggct	2280
attaagattc	ttaatgagac	aactgggtccc	aaggcaaagt	tggagttcat	ggatgaagct	2340
ctgatcatgg	caagtatgga	tcatccacac	ctagtccggg	tgctgggtgt	gtgtctgagc	2400
ccaaccatcc	agctggttac	tcaacttatg	ccccatggct	gcctgttgga	gtatgtccac	2460
gagcacaagg	ataacattgc	atcacacatc	ctgcttaact	ggtgtgtcca	gatagtcaag	2520
ggaatcatgt	acctggaaga	aagacgactc	gttcattcggg	atttggcagc	ccgtaaatgc	2580
ttagtgaat	ctccaaacca	tgtgaaaatc	acagattttg	ggctagccag	actcttgga	2640
ggagatgaaa	aagagtacaa	tgtctgatgga	ggaaagatgc	caattaaaatg	gatggctctg	2700
gagtgataac	attacaggaa	attcacccat	cagagtgcag	tttgagagcta	tggagttact	2760
atatgggaac	tgatgacctt	tggaggaaaa	ccctatgatg	gaattccaac	gcgagaaatc	2820
cctgatttat	tagagaaagg	agaacgtttg	cctcagcctc	ccatctgcac	tattgacgtt	2880
tacatggcca	tgggtcaaatg	ttggatgatt	gatgctgaca	gtagacctaa	atttaaggaa	2940
ctggctgctg	agttttcaag	gatggctcga	gacctcaaa	gatacctagt	tattcagggg	3000
gatgatcgta	tgaagcttcc	cagtccaaat	gacagcaagt	tctttcagaa	tctcttggat	3060
gaagaggatt	tggaagatat	gatggatgct	gaggagtact	tggtcctcca	ggctttcaac	3120
atcccacctc	ccatctatac	ttccagagca	agaattgact	cgaataggag	tgaattgga	3180
cacagccctc	ctcctgccta	cacccccatg	tcaggaaacc	agtttgtata	ccgagatgga	3240
ggttttgctg	ctgaacaagg	agtgtctgtg	ccctacagag	ccccacttag	cacaattcca	3300
gaagctcctg	tggcacaggg	tgctactgct	gagatttttg	atgactcctg	ctgtaatggc	3360
accctacgca	agccagtggc	accccattgc	caagaggaca	gtagcaccca	gaggtacagt	3420
gctgacccca	ccgtgtttgc	cccagaacgg	agcccacgag	gagagctgga	tgaggagaagt	3480
tacatgactc	ctatgcgaga	caaacccaaa	caagaatacc	tgaatccagt	ggagagaaac	3540
cctttttgtt	ctcggagaaa	aaatggagac	cttcaagcat	tggataatcc	cgaatatcac	3600
aatgcatcca	atgggtccacc	caaggccgag	gatgagtatg	tgaatgagcc	actgtacctc	3660
aacacctttg	ccaacacctt	gggaaaagct	gagtacctga	agaacaacat	actgtcaatg	3720
ccagagaagg	ccaagaaagc	gtttgacaac	cctgactact	ggaaccacag	cctgccacct	3780
cggagcaccc	ttcagcaccc	agactacctg	caggagtaca	gcacaaaata	tttttataaa	3840
cagaatgggc	ggatccggcc	tattgtggca	gagaatcctg	aatacctctc	tgagttctcc	3900
ctgaagccag	gcactgtgct	gccgcctcca	ccttacagac	accggaatac	tgtgggtgta	3960
gctcagttgt	ggtttttttag	gtggagagac	acacctgctc	caatttcccc	acccccctct	4020
ctttctctgg	tggcttccct	tctaccccaa	ggccagtagt	tttgacactt	cccagtgga	4080
gatacacaga	tgcaatgata	gttatgtgct	tacctaaact	gaacattaga	gggaaagact	4140
gaaagagaaa	gataggagga	accacaatgt	ttcttcattt	ctctgcatgg	gttggtcagg	4200
agaatgaaac	agctagagaa	ggaccagaaa	atgtaaggca	atgctgccta	ctatacaact	4260
agctgtcact	ttttttcttt	ttctttttct	tcttttggtt	ctttcttctc	cttctttttt	4320
tttttttttt	taaagcagat	ggttgaacaa	cccatgctat	ctgttctcat	ctgcaggaac	4380
tgatgtgtgc	atattttagca	tccctggaaa	tcataataaa	gtttccatta	gaacaaaaga	4440
ataacatttt	ctataacata	tgatagtgtc	tgaatttgag	aatccagttt	ctttccccag	4500
cagttttctgt	cctagcaagt	aagaatggcc	aactcaactt	tcataattta	aaaatctcca	4560
ttaaagttaa	aactagtaat	tatgttttca	acactttttg	gttttttttca	ttttgttttg	4620
ctctgaccga	ttcctttata	tttgctcccc	tattttttgg	tttaattttct	aattgcaaag	4680
atgtttacat	caaagcttct	tcacagaatt	taagcaagaa	atattttta	atagtgaat	4740
ggccactact	ttaagtatac	aatcttttaa	ataagaaagg	gaggctaata	tttttcatgc	4800
tatcaaatta	tcttcacctt	catcctttac	atttttcaac	attttttttt	ctccataaat	4860
gacactactt	gataggccgt	tggttgtctg	aagagtagaa	gggaaactaa	gagacagttc	4920
tctgtggttc	aggaaaacta	ctgatacttt	caggggtggc	ccaatgaggg	aatccattga	4980
actggaagaa	acacactgga	ttgggtatgt	ctacctggca	gatactcaga	aatgtagttt	5040
gcaattaaag	tgaattttta	tttgttcttt	ttctgaactc	cattttggat	tttgaatcaa	5100
gcaatatgga	agcaaccagc	aaatttaacta	atttaagtac	attttttaaaa	aaagagctaa	5160
gataaagact	gtggaatgc	caaaccaaag	aaatttaggaa	ccttgcaacg	gtatccaagg	5220

			355						360						365					
Leu	Val	Thr	Gly	Ile	His		Gly	Asp	Pro	Tyr	Asn	Ala	Ile	Glu	Ala	Ile				
	370						375					380								
Asp	Pro	Glu	Lys	Leu	Asn		Val	Phe	Arg	Thr	Val	Arg	Glu	Ile	Thr	Gly				
385					390						395					400				
Phe	Leu	Asn	Ile	Gln	Ser	Trp	Pro	Pro	Asn	Met	Thr	Asp	Phe	Ser	Val					
				405					410					415						
Phe	Ser	Asn	Leu	Val	Thr	Ile	Gly	Gly	Arg	Val	Leu	Tyr	Ser	Gly	Leu					
			420				425						430							
Ser	Leu	Leu	Ile	Leu	Lys	Gln	Gln	Gly	Ile	Thr	Ser	Leu	Gln	Phe	Gln					
		435				440						445								
Ser	Leu	Lys	Glu	Ile	Ser	Ala	Gly	Asn	Ile	Tyr	Ile	Thr	Asp	Asn	Ser					
	450					455					460									
Asn	Leu	Cys	Tyr	Tyr	His		Thr	Ile	Asn	Trp	Thr	Thr	Leu	Phe	Ser	Thr				
465					470						475					480				
Ile	Asn	Gln	Arg	Ile	Val	Ile	Arg	Asp	Asn	Arg	Lys	Ala	Glu	Asn	Cys					
				485					490					495						
Thr	Ala	Glu	Gly	Met	Val	Cys	Asn	His	Leu	Cys	Ser	Ser	Asp	Gly	Cys					
			500					505					510							
Trp	Gly	Pro	Gly	Pro	Asp	Gln	Cys	Leu	Ser	Cys	Arg	Arg	Phe	Ser	Arg					
		515				520						525								
Gly	Arg	Ile	Cys	Ile	Glu	Ser	Cys	Asn	Leu	Tyr	Asp	Gly	Glu	Phe	Arg					
	530					535					540									
Glu	Phe	Glu	Asn	Gly	Ser	Ile	Cys	Val	Glu	Cys	Asp	Pro	Gln	Cys	Glu					
545				550						555					560					
Lys	Met	Glu	Asp	Gly	Leu	Leu	Thr	Cys	His	Gly	Pro	Gly	Pro	Asp	Asn					
			565						570					575						
Cys	Thr	Lys	Cys	Ser	His	Phe	Lys	Asp	Gly	Pro	Asn	Cys	Val	Glu	Lys					
			580					585					590							
Cys	Pro	Asp	Gly	Leu	Gln	Gly	Ala	Asn	Ser	Phe	Ile	Phe	Lys	Tyr	Ala					
		595					600					605								
Asp	Pro	Asp	Arg	Glu	Cys	His	Pro	Cys	His	Pro	Asn	Cys	Thr	Gln	Gly					
	610					615					620									
Cys	Asn	Gly	Pro	Thr	Ser	His	Asp	Cys	Ile	Tyr	Tyr	Pro	Trp	Thr	Gly					
625					630					635					640					
His	Ser	Thr	Leu	Pro	Gln	His	Ala	Arg	Thr	Pro	Leu	Ile	Ala	Ala	Gly					
				645					650					655						
Val	Ile	Gly	Gly	Leu	Phe	Ile	Leu	Val	Ile	Val	Gly	Leu	Thr	Phe	Ala					
			660					665					670							
Val	Tyr	Val	Arg	Arg	Lys	Ser	Ile	Lys	Lys	Lys	Arg	Ala	Leu	Arg	Arg					
		675					680					685								
Phe	Leu	Glu	Thr	Glu	Leu	Val	Glu	Pro	Leu	Thr	Pro	Ser	Gly	Thr	Ala					
	690					695					700									

Ser	Gln	Leu	Leu	Leu	Asn	Trp	Cys	Val	Gln	Ile	Ala	Lys	Gly	Met	Met		
			820					825					830				
Tyr	Leu	Glu	Glu	Arg	Arg	Leu	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn		
		835					840					845					
Val	Leu	Val	Lys	Ser	Pro	Asn	His	Val	Lys	Ile	Thr	Asp	Phe	Gly	Leu		
		850				855					860						
Ala	Arg	Leu	Leu	Glu	Gly	Asp	Glu	Lys	Glu	Tyr	Asn	Ala	Asp	Gly	Gly		
865				870						875					880		
Lys	Met	Pro	Ile	Lys	Trp	Met	Ala	Leu	Glu	Cys	Ile	His	Tyr	Arg	Lys		
			885						890					895			
Phe	Thr	His	Gln	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr	Ile	Trp	Glu		
		900					905						910				
Leu	Met	Thr	Phe	Gly	Gly	Lys	Pro	Tyr	Asp	Gly	Ile	Pro	Thr	Arg	Glu		
		915				920						925					
Ile	Pro	Asp	Leu	Leu	Glu	Lys	Gly	Glu	Arg	Leu	Pro	Gln	Pro	Pro	Ile		
	930					935					940						
Cys	Thr	Ile	Asp	Val	Tyr	Met	Val	Met	Val	Lys	Cys	Trp	Met	Ile	Asp		
945				950						955					960		
Ala	Asp	Ser	Arg	Pro	Lys	Phe	Lys	Glu	Leu	Ala	Ala	Glu	Phe	Ser	Arg		
			965					970						975			
Met	Ala	Arg	Asp	Pro	Gln	Arg	Tyr	Leu	Val	Ile	Gln	Gly	Asp	Asp	Arg		
		980					985						990				
Met	Lys	Leu	Pro	Ser	Pro	Asn	Asp	Ser	Lys	Phe	Phe	Gln	Asn	Leu	Leu		
	995					1000						1005					
Asp	Glu	Glu	Asp	Leu	Glu	Asp	Met	Met	Asp	Ala	Glu	Glu	Tyr	Leu	Val		
	1010					1015					1020						
Pro	Gln	Ala	Phe	Asn	Ile	Pro	Pro	Pro	Ile	Tyr	Thr	Ser	Arg	Ala	Arg		
1025				1030						1035					1040		
Ile	Asp	Ser	Asn	Arg	Ser	Glu	Ile	Gly	His	Ser	Pro	Pro	Pro	Ala	Tyr		
			1045					1050						1055			
Thr	Pro	Met	Ser	Gly	Asn	Gln	Phe	Val	Tyr	Arg	Asp	Gly	Gly	Phe	Ala		
		1060					1065						1070				
Ala	Glu	Gln	Gly	Val	Ser	Val	Pro	Tyr	Arg	Ala	Pro	Thr	Ser	Thr	Ile		
	1075					1080					1085						
Pro	Glu	Ala	Pro	Val	Ala	Gln	Gly	Ala	Thr	Ala	Glu	Ile	Phe	Asp	Asp		
	1090					1095					1100						
Ser	Cys	Cys	Asn	Gly	Thr	Leu	Arg	Lys	Pro	Val	Ala	Pro	His	Val	Gln		
1105			1110							1115					1120		
Glu	Asp	Ser	Ser	Thr	Gln	Arg	Tyr	Ser	Ala	Asp	Pro	Thr	Val	Phe	Ala		
			1125						1130					1135			
Pro	Glu	Arg	Ser	Pro	Arg	Gly	Glu	Leu	Asp	Glu	Glu	Gly	Tyr	Met	Thr		
		1140					1145						1150				
Pro	Met	Arg	Asp	Lys	Pro	Lys	Gln	Glu	Tyr	Leu	Asn	Pro	Val	Glu	Glu		
	1155					1160						1165					
Asn	Pro	Phe	Val	Ser	Arg	Arg	Lys	Asn	Gly	Asp	Leu	Gln	Ala	Leu	Asp		
	1170					1175					1180						
Asn	Pro	Glu	Tyr	His	Asn	Ala	Ser	Asn	Gly	Pro	Pro	Lys	Ala	Glu	Asp		
1185			1190							1195					1200		
Glu	Tyr	Val	Asn	Glu	Pro	Leu	Tyr	Leu	Asn	Thr	Phe	Ala	Asn	Thr	Leu		
		1205							1210					1215			
Gly	Lys	Ala	Glu	Tyr	Leu	Lys	Asn	Asn	Ile	Leu	Ser	Met	Pro	Glu	Lys		
		1220					1225						1230				
Ala	Lys	Lys	Ala	Phe	Asp	Asn	Pro	Asp	Tyr	Trp	Asn	His	Ser	Leu	Pro		
	1235						1240					1245					
Pro	Arg	Ser	Thr	Leu	Gln	His	Pro	Asp	Tyr	Leu	Gln	Glu	Tyr	Ser	Thr		
	1250					1255					1260						
Lys	Tyr	Phe	Tyr	Lys	Gln	Asn	Gly	Arg	Ile	Arg	Pro	Ile	Val	Ala	Glu		

<210> 4
 <211> 615
 <212> PRT
 <213> Homo sapiens

<400> 4

Gln	Ser	Val	Cys	Ala	Gly	Thr	Glu	Asn	Lys	Leu	Ser	Ser	Leu	Ser	Asp
1				5					10					15	
Leu	Glu	Gln	Gln	Tyr	Arg	Ala	Leu	Arg	Lys	Tyr	Tyr	Glu	Asn	Cys	Glu
		20						25					30		
Val	Val	Met	Gly	Asn	Leu	Glu	Ile	Thr	Ser	Ile	Glu	His	Asn	Arg	Asp
	35					40					45				
Leu	Ser	Phe	Leu	Arg	Ser	Val	Arg	Glu	Val	Thr	Gly	Tyr	Val	Leu	Val
	50				55					60					
Ala	Leu	Asn	Gln	Phe	Arg	Tyr	Leu	Pro	Leu	Glu	Asn	Leu	Arg	Ile	Ile
65				70					75					80	
Arg	Gly	Thr	Lys	Leu	Tyr	Glu	Asp	Arg	Tyr	Ala	Leu	Ala	Ile	Phe	Leu
			85					90					95		
Asn	Tyr	Arg	Lys	Asp	Gly	Asn	Phe	Gly	Leu	Gln	Glu	Leu	Gly	Leu	Lys
		100						105					110		
Asn	Leu	Thr	Glu	Ile	Leu	Asn	Gly	Gly	Val	Tyr	Val	Asp	Gln	Asn	Lys
	115					120						125			
Phe	Leu	Cys	Tyr	Ala	Asp	Thr	Ile	His	Trp	Gln	Asp	Ile	Val	Arg	Asn
	130					135				140					
Pro	Trp	Pro	Ser	Asn	Leu	Thr	Leu	Val	Ser	Thr	Asn	Gly	Ser	Ser	Gly
145				150					155						160
Cys	Gly	Arg	Cys	His	Lys	Ser	Cys	Thr	Gly	Arg	Cys	Trp	Gly	Pro	Thr
			165					170					175		
Glu	Asn	His	Cys	Gln	Thr	Leu	Thr	Arg	Thr	Val	Cys	Ala	Glu	Gln	Cys
		180						185					190		
Asp	Gly	Arg	Cys	Tyr	Gly	Pro	Tyr	Val	Ser	Asp	Cys	Cys	His	Arg	Glu
	195					200					205				
Cys	Ala	Gly	Gly	Cys	Ser	Gly	Pro	Lys	Asp	Thr	Asp	Cys	Phe	Ala	Cys
	210				215					220					
Met	Asn	Phe	Asn	Asp	Ser	Gly	Ala	Cys	Val	Thr	Gln	Cys	Pro	Gln	Thr
225				230					235					240	
Phe	Val	Tyr	Asn	Pro	Thr	Thr	Phe	Gln	Leu	Glu	His	Asn	Phe	Asn	Ala
			245					250						255	
Lys	Tyr	Thr	Tyr	Gly	Ala	Phe	Cys	Val	Lys	Lys	Cys	Pro	His	Asn	Phe
		260					265						270		
Val	Val	Asp	Ser	Ser	Ser	Cys	Val	Arg	Ala	Cys	Pro	Ser	Ser	Lys	Met
	275					280						285			
Glu	Val	Glu	Glu	Asn	Gly	Ile	Lys	Met	Cys	Lys	Pro	Cys	Thr	Asp	Ile
	290				295						300				
Cys	Pro	Lys	Ala	Cys	Asp	Gly	Ile	Gly	Thr	Gly	Ser	Leu	Met	Ser	Ala
305				310					315					320	
Gln	Thr	Val	Asp	Ser	Ser	Asn	Ile	Asp	Lys	Phe	Ile	Asn	Cys	Thr	Lys
			325					330					335		
Ile	Asn	Gly	Asn	Leu	Ile	Phe	Leu	Val	Thr	Gly	Ile	His	Gly	Asp	Pro
	340						345						350		
Tyr	Asn	Ala	Ile	Glu	Ala	Ile	Asp	Pro	Glu	Lys	Leu	Asn	Val	Phe	Arg
	355					360					365				
Thr	Val	Arg	Glu	Ile	Thr	Gly	Phe	Leu	Asn	Ile	Gln	Ser	Trp	Pro	Pro
	370				375						380				
Asn	Met	Thr	Asp	Phe	Ser	Val	Phe	Ser	Asn	Leu	Val	Thr	Ile	Gly	Gly
385				390					395					400	

054050-000000

